

Docket No.: 7682-109-999 Serial No.: 10/722,050

Inventor(s): Spaete et al.
Title: "NON-SPLICING VARIANTS OF GP350/220"

MetGluAlaAlaLeuLeuValCysGlnTyrThrIleGlnSerLevIleHisLevThrGly 20 -900 TCTGTACAATGTTACCCACGGAGCTCTGAACATACAACCACTGGCGATCCCCGGGGGTACATCGCGGCGTTAAAGGTGCCGGCGGAAAAGGTCACGTGACGTGACGTACGGCCACCTGTGC -780 ACCCAAGTGTCGCCTGGAGATGTAGGAATGTGGGAGTCGTCTGGTGATCGGTGTAGCTGTACATCCAGCTGCTGTATGCCCTGGTAGGCCATAGGCCATCGGCGGCGTTTGCAGTC -660 ICCATTIGGCCTGATCTCTAGGAGAAGCTGGATTTCTCCGACGATCTCTAATGGCCTGTCGAATGGCCATGGCATACATTATGTACATCTGGATTTTGAAATCTGGATCTGGAAAAACTG -1013 EcoR] GAATTCCATAAATGAAACACGCTGGTCAGGTGTTAAAACTTCCTCCCAGATTTTCGTGAGGCTCCTGTGTATAGCCATATAGTCAAAGAAAATACTGTAGCGGGGATTACAGC -300 CATCATGATCGACCCGCTTTCTCTTCGTACCCTTCTGGGCCGGCTCCAGGTGGGCATCTTCTGCTTTTCTGAGCTGCTATCTGATAACTCTATGAGGACATTTTCCCAATCTCCCG

GluAspProGlyPhePheAsnValGluIleProGluPheProPheTyrProThrCysAsnValCysThrAlaAspValAsnValThrIleAsnPheAspValGlyGlyLysLysHisGln 60 61 GAAGATCCTGGTTTTTCAATGTTGAGATTCCGGAATTCCCATTTTACCCCACATGCTTTGCACGCCAGATGTCAATGTAACTATCAATTTCGATGTCGGGGGGGAAAAGCATCAA

LeuAspLeuAspPheGlyGlnLeuThrProHisThrLysAlaValTyrGlnProArgGlyAlaPheGlyGlySerGluAsnAlaThrAsnLeuPheLeuLeuGluLeuLeuGlyAlaGly 100 CTIGATCTICACTTICCCCACCTCACACCCCATACCAAGCTGTCTACCAACCTCGAGGTGCATTICGTGGTCGCTCAGAAAATGCCCACCAATCTTTCTACTGCAGCTCCTTGGTGCAGGA <u>~</u>

GluLeuAlaLeuThrMetArgSerLysLysLeuProIleAsnValThrThrGlyGluGluGlnGInValSerLeuGluSerValAspValTyrPheGlnAspValPheGlyThrMetTrp 140 GAATTGGCTCTAACTATGCGGTCTAAGAAGCTTCCAATTAACGTCACCACCGGAGAGGAGCAACAAGTAAGCCTCGGAATCTGTAGATGTCTACTTTCAAGATGTGTTTGGAACCATGTGG 300

CysHisHisAlaGluMetGlnAsnProValTyrLeuIleProGluThrValProTyrIleLysTrpAspAsnCysAsnSerThrAsnIleThrAlaValValArgAlaGlnGlyLeuAsp 180

VolThrLeuProLeuSerLeuProThrSerAlaGlnAspSerAsnPheSerValLysThrGluMetLeuGlyAsnGlulleAsplleGluCysIleMetGluAspGlyGlulleSerGln 220 541 GTCACGCTACCCTTAAGTTTGCCAACGTCAGCTCCAAGACTCGAATTTCAGCGTAAAAACAGAAATGCTCGGTAATGAGATAGTAGTGTATTATGGAGGATGGCGAAATTTCACAA

ValLeuProGlyAspAsnLysPheAsnIleThrCysSerGlyTyrGluSerHisValProSerGlyGlyIleLeuThrSerThrSerProValAlaThrProIleProGlyThrGlyTyr 260 661 GTTCTGCCCGGAGACAACAATTTAACATCACCTGCAGTGGATACGAGAGCCATGTTCCCAGCGGGGGAATTCTCACATCAACGAGTCCCGTGGCCACCCCAATACCTGGTACAGGGTAT

FIG. 1/

- SerAsnileValPheSerAspGlulleProAlaSerGlnAspMetProThrAsnThrThrAsplleThrTyrValGlyAspAsnAlaThrTyrSerValProMetValThrSerGluAsp 340 TCCAACATIGITICTCTGATGAGATTCCAGCTTCACAGGACATGCCGACAAACACCACAGACATCACATATGTGGGGTGACATGCTACTATTCAGTGCCAATGGTCACTTCTGAGGGAC
- 380 AlaAsnSerProAsnValThrValThrAlaPheTrpAlaTrpProAsnAsnThrGluThrAspPheLysCysLysTrpThrLeuThrSerGlyThrProSerGlyCysGluAsnIleSer 021 GCAAACTCGCCAAATGTTACAGTGACTGCCTTTTGGGCCTGGCCAAACAACACTGAAACTGACTTTAAGTGCAAATGGACTCTCACCTCGGGGACACCTTCGGGTTGTGAAATATTTCT
- GlyAlaPheAlaSerAsnArgThrPheAspIleThrValSerGlyLeuGlyThrAlaProLysThrLeuIleIleThrArgThrAlaThrAsnAlaThrThrThrThrHisLysValIle 420 141 GGTGCATTIGCGAGCAATGGCACATTGACATTACTGTCTGGGGTCTTGGCACGCCCCCAAGACACTCATTATCACAGGAAGGCTACCAATGCCACCACCAACAACGTTATA
- 460 PheSerLysAIaProGiuSerThrThrThrSerProThrLeuAsnThrThrGiyPheAIaAspProAsnThrThrGiyLeuProSerSerThrHisVaIProThrAsnLeuThrAia 261 TICTCCAAGGCACCCCAGAGCACCACCACCTCCCCTACCTTGAATACAACTGGATTTGCTGATCCCAATACAACGACGAGGTCTACCCAGGTCTACTCACGTGCCTACCAACCTCACCGCA
- ProAlaSerThrGlyProThrValSerThrAlaAspValThrSerProThrProAlaGlyThrThrSerGlyAlaSerProValThrProSerProSerProTrpAspAsnGlyThrGlu 500 381
- 540 SerlysAalProAspMetThrSerSerThrSerProValThrProThrProAsnAlaThrSerProThrProAlaValThrThrProAsnAlaThrSerProThrProAla 50
- 280 ValThrThrProThrProAsnAlaThrSerProThrLeuGlyLysThrSerProThrSerAlaValThrThrProThrProAsnAlaThrSerProThrLeuGlyLysThrSerProThr 621
- 620 SerAlayalThrThrProIhrProAsnAlaThrSerProThrLeuGlyLysThrSerProThrSerAlayalThrThrProAsnAlaThrGlyProThrValGlyGluThrSer TCAGCAGTGACTACCCCAACCCCAAATGCCACCACCACCCTGGGAAAAACAAGCCCCACCTCAGCAGTGACTACCCCAAACCAAATGCCACGGGCCCTACTGTGGGAGAAACAAGT 741
- 99 <u>ProGInAlaAsnAlaThrAsnHisThrLeuGlyGlyThrSerProThrProValValThrSer</u>GlnProLysAsnAlaThrSerAlaValThrThrGlyGlnHisAsnIleThrSerSer CCACAGGCAAATGCCACCACCACACCTTAGGAGGAACAAGTCCCACCCCAGTAGTTACCAGCCAAAAAAATGCAACCAGTGCTGTTACCACGGGCCAACATAACATAACTTCAAGT 861

ACCEPTOR -

- AsnileThrGInVaIThrProAlaSerIleSerThrHisHisValSerThrSerSerProGluProArgProGlyThrThrSerGInAlaSerGlyProGlyAsnSerSerThrSerThr 740 2101 AATATAACACGGTGACACCAGCCTCTATCAGCACATCATGTGTGTCTCCCCAGTTCGCCCAGACCCCGCCCAGGCACCCAGCCTTCAGCCCTGGAAACAGTTCCACATCCACA
- LysProG1yG1uVa1AsnVa1ThrLysG1yThrProProG1nAsnA1aThrSerProG1nA1aProSerG1yG1nLysThrA1aVa1ProThrVa1ThrSerThrG1yG1yLysA1aAsn 780 2221 AAACCGGGGGGGGTTAATGTCACCAAAGGCACGCCCCCCCAAAATGCAACGTCGCCCCCAGGCCCCCAAAAGACGCCGCGTTCCCACGGTCACCTCAACAGGTGGAAAGGCCAAT
- SerThrThrG1yG1yLysHisThrThrG1yHisG1yAlaArgThrSerThrG1uProThrThrAspTyrG1yG1yAspSerThrThrProArgProArgTyrAsnAlaThrThrTyrLeu 820 2341 TCTACCACCGGTGGAAAGCACACCACAGGACATGGAGCCCGGACAAGTACAGAGCCCACCACAGATTACGGCGGTGATTCAACTACGCCAAGACCGAGATACAATGCGACCACCTATCTA
- ProProSerThrSerSerLysLeuAagProArgTrpThrPheThrSerProProValThrThrAlaGInAlaThrValProValProProThrSerGInProArgPheSerAsnLeuSer 860 2461 CCICCCAGCACTICTAGCAAACTGCGGCCCCGCTGGACTTTTACGAGCCCACCGGTTACCACACCCCAAGCCACCGTGCCAGTCCCGCCAACGTCCCAGCCCAGGTTCTCAAACCTCTC
- MetLeuVaiLeuGinTrpAiaSerLeuAiaVaiLeuThrLeuLeuLeuLeuLeuVaiMetAidAspCysAiaPheArgArgAsnLeuSerThrSerHisThrTyrThrThrProProTyr 900
- 2701 GATGACGCCGAGACCTATGTATAAAGTCAATAAAAATTTATTAATCAGAAATTTGCACTTTGCTTCACGTCCCCGGGAGCGGGGGCGCGCCTCCGTTGCGTTGCGTTTGCTTTG POL YA AspAspAloGluThrTyrVal***
- 2821 ATTCTCGTGGTCGTGTTCCCTCACCAGGGCTGGGTTGCCCTTTTGCACCCCAACATAGATACTTGAATGCGGAGGGTCAGATTTTGCAATATATTTTCCATTTCATTGCGGGTAGTTACACAC 2941 CGICAACAGATIICCGAACCIIGICIICAAICIICAIAGCCIGAGACGCCGAAACGCCCGIGCCIGCGIAAICAIIACCICICGCIGICGAGCIGIAAGCGGCTCAGGCGGCTCAGGCGGCTCAGGCGGCTCAGGCGCTCAGGCGCTCAGGCGCTCAGGCGCTCAGGCGCTCAGGCGCTCAGGCGCAGGCAA
 - 3181 TGTCAACACCCTTAACAGAAGCCAATCTGACTTTGCGTGGAGCTGATTGCTTTAACGAGCAGAAGAAGTACAAACAGCCGAGATTGCTGCCCCTTTTAAATATCCCCATCT
- AATCCGTCAGCAGCGTGFTCACAAACTTGTTAAAGCAGACGTACATCAGGTAGATGGCTGAGGCTATAATGACTAAGACAAGCGTCAGAAGTGCCCAGATGGAGGCCAAAAGCTGGTGGTGGTGGAGGCTGGTCAAAG
 - 3421
 - TGTCTGTTAGATCATCACCATGGAGGCCTGTCCACACATACGCTACGCCTTCCAGAATGACAAGCTGTTGCTCCAGCAGGCTAGTGTAGGGCGGCTCACCTTGGTCAACAAGACCACCAT

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AGGCACCGGTCTCGTCCATCTTGAGCGCCGTGGCCACCTTCTCCATCTCAGGGCCCAGGCCTGTCGCCAGCCTGTTTGTCCAGCAGGGCCTTGAGCCCATTCTCGTCCATCTCGATGC CATCGATCCCGGCTACACGGGGGAACTCCGGGCTAATCCTCCAGAATCAGCGGGGCTACAACTCCACGCTGCGTCCATCGGAGCTCAAAATCCACCTGGCTGCCTTCAGATATGCCACCC CACCETECCCCCCCTTCTATCCCTCACCACAGGCCGACAATCTTTGGCAGGTCGGGCCTGGCCATGCAGGGTATTCTAGTGAAGCCCTGCAGGTGGCGCCGGGGTGGGGTTGGGGTGGGGTTCAG CCTGACCAACTTTAGTGACCAGACGGTGTTCCTTAACAAGTACGGGGGCTTCTGTCAGCTTGTTTACCTTCACAAGCACCACCTCACCTCCTTCTACAGCCCCCACAGTGACGCGGGGGT CCTTGCCCCCAGATCTCTCTTTAGGTGGGCCAGCTGCACCTTCGAGGAGGTGCCGAGCCTGGCCATGGGTGATAGTGGGCTGAGCGAGGCGCTCGAGGGGAGACAGGGGAAGAGGGGGTTTTGG CCAGATGGAGGAGACAAGGGTCCCATCAACCACCCCCAGTACCCCGGGGACGTGGGCCTGGACGTCTTTGCCAAAGGACCTGGCCCTCTTCCCCATCAGACCGTCTCAGTGACACT CCCTTACAGCCAGAGAGATCATGGTATTCCAGATGACTGAGCGCCACGGCCTCAAGCTT HINDIII 4021 4141 4261 4501 4381

FIG. 1D



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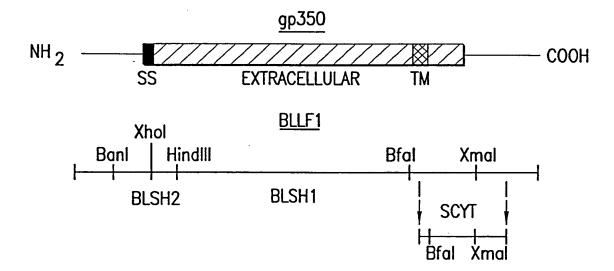


FIG. 2A

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BLSH2 BLSH 1 BLSH 1 Banl Bfal HindIII SCYT Xbal--Bfal HindIII. pSTG3 HindIII pSTG1 -Xmal pSTG2 -EcoRI pMT11 pMT11 pMT11 HindIII HindIII Bfal Banl Banl Bfal XbalpDTM Xbal -Xmal **pSTOP** EcoRI pEE14 pEE14 Xhol M13DTM -BamHI OR Asp718I M13STOP **MUTAGENESIS** HindIII HindIII Banl -Bfal Bfal Banl pMDTM Xbal pMSTOP Xbal--Xmal **EcoRI**

FIG. 2B

pEE14

pEE14

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